Application No.: 09/50 8 9 NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

ĺow	ing reason(s):
X	 This application clearly fails to comply with the requirements of 37 C.F.R. 1,821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
X	2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
M	3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
	4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."
	5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
	6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
	7. Other:
Applicant Must Provide:	
\ X	An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
X	An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
N	A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).
Foi	questions regarding compliance to these requirements, please contact:
-	20da 1 da 1

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

For Patentin software help, call (703) 308-6856

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

SEQUENCE LISTING

<110> Miyata, Toshio

<120> MEGSIN PROTEIN

<130> SHIM004

<140>09/508,997

<141> 2000.06.27

<150> PCT/JP98/04269

<151> 1998-09-22

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Asp Ser Leu Ser Gln lie Asp Lys Leu Leu His Val Asn Thr Ala Ser 50 55 60

Gly Tyr Gly Asn Ser Ser Asn Ser Gln Ser Gly Leu Gln Ser Gln Leu 65 70 75 80

Lys Arg Val Phe Ser Asp Ile Asn Ala Ser His Lys Asp Tyr Asp Leu 85 90 95

Ser lie Val Asn Gly Leu Phe Ala Glu Lys Val Tyr Gly Phe His Lys 100 105 110

Asp Tyr Ile Glu Cys Ala Glu Lys Leu Tyr Asp Ala Lys Val Glu Arg 115 120 125

Val Asp Phe Thr Asn His Leu Glu Asp Thr Arg Arg Asn Ile Asn Lys 130 135 140

Trp Val Glu Asn Glu Thr His Gly Lys Ile Lys Asn Val Ile Gly Glu 145 150 155 160

Gly Gly Ile Ser Ser Ser Ala Val Met Val Leu Val Asn Ala Val Tyr 165 170 175

Phe Lys Gly Lys Trp Gln Ser Ala Phe Thr Lys Ser Glu Thr lle Asn 180 185 190

Cys His Phe Lys Ser Pro Lys Cys Ser Gly Lys Ala Val Ala Met Met 195 200 205

His Gln Glu Arg Lys Phe Asn Leu Ser Val IIe Glu Asp Pro Ser Met 210 215 220

Lys lle Leu Glu Leu Arg Tyr Asn Gly Gly lle Asn Met Tyr Val Leu 225 230 235 240

Leu Pro Glu Asn Asp Leu Ser Glu lle Glu Asn Lys Leu Thr Phe Gln 245 250 255

Asn Leu Met Glu Trp Thr Asn Pro Arg Arg Met Thr Ser Lys Tyr Val 260 265 270

Glu Val Phe Phe Pro Gln Phe Lys Ile Glu Lys Asn Tyr Glu Met Lys 275 280 285

Gin Tyr Leu Arg Ala Leu Gly Leu Lys Asp Ile Phe Asp Glu Ser Lys 290 295 300

Ala Asp Leu Ser Gly lle Ala Ser Gly Gly Arg Leu Tyr lle Ser Arg

320 315 305 310 Met Met His Lys Ser Tyr lle Glu Val Thr Glu Glu Gly Thr Glu Ala 330 335 325 Thr Ala Ala Thr Gly Ser Asn Ile Val Glu Lys Gln Leu Pro Gln Ser 350 340 345 Thr Leu Phe Arg Ala Asp His Pro Phe Leu Phe Val Ile Arg Lys Asp 360 365 Asp IIe IIe Leu Phe Ser Gly Lys Val Ser Cys Pro 375 370

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Asp Cys Xaa Arg Gln Ile Asp Lys Ala Leu His Phe Ile Ser Pro Ser 50 55 60

Arg Gin Gly Asn Ser Ser Asn Ser Gin Leu Gly Leu Gin Tyr Gin Leu 65 70 75 80

Lys Arg Val Leu Ala Asp Ile Asn Ser Ser His Lys Asp Xaa Lys Leu 85 90 95

Ser Ile Ala Asn Gly Val Phe Ala Glu Lys Val Phe Asp Phe His Lys 100 105 110

Ser Tyr Met Giu Cys Ala Giu Asn Leu Tyr Asn Ala Lys Val Giu Arg 115 120 125

Val Asp Phe Thr Asn Asp Ile Gln Glu Thr Arg Phe Lys Ile Asn Lys 130 135 140

Trp Ile Glu Asn Glu Thr His Gly Lys Ile Lys Lys Val Leu Gly Asp 145 150 155 160

Ser Ser Leu Ser Ser Ser Ala Val Met Val Leu Val Asn Ala Val Tyr 165 170 175

Phe Lys Gly Lys Trp Lys Ser Ala Phe Thr Lys Ser Asp Thr Leu Ser 180 185 190

Cys His Phe Arg Ser Pro Ser Gly Pro Gly Lys Ala Val Asn Met Met 195 200 205

His Gln Glu Arg Arg Phe Asn Leu Ser Thr Ile Gln Glu Pro Pro Met 210 215 220

Gin Ile Leu Glu Leu Gin Tyr His Gly Gly Ile Ser Met Tyr Ile Met 225 230 235 240

Leu Pro Glu Asp Asp Leu Ser Glu Ile Glu Ser Lys Leu Ser Phe Gln 245 250 255

Asn Leu Met Asp Trp Thr Asn Ser Arg Lys Met Lys Ser Gln Tyr Val 260 265 270

Asn Val Phe Leu Pro Gln Phe Lys Ile Glu Lys Asp Tyr Glu Met Arg 275 280 285

Ser His Leu Lys Ser Val Gly Leu Glu Asp lle Phe Val Glu Ser Arg 290 295 300

Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Val Ser Lys 305 310 315 320

Leu Met His Lys Ser Leu IIe Glu Val Ser Glu Glu Gly Thr Glu Ala 325 330 335

Thr Ala Ala Thr Glu Ser Asn Ile Val Glu Lys Leu Leu Pro Glu Ser 340 345 350

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<223> Synthesis

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<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesis

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27

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